

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2003, 09:35:03 ; Search time 35 seconds

(without alignment)
2307.728 Million cell updates/sec

Title: US-09-935-124a-2

Perfect score: 2018
Sequence: 1 MDLFGDLPPEPSPPPAAGK.....KAVQSGADNTVMVRIQH 392

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2018	100.0	382	4 Q9H0C8	Q9H0C8 homo sapien
2	1935	95.9	382	11 Q8R0K6	Q8R0K6 mus musculi
3	1931	95.7	382	11 Q8R0K6	Q8R0K6 mus musculi
4	1886	68.7	272	11 Q8D0C9	Q8D0C9 mus musculi
5	1078	53.4	212	11 Q8C546	Q8C546 mus musculi
6	856	42.4	167	11 Q8Z0T2	Q8Z0T2 mus musculi
7	481	23.8	341	10 Q9LMT1	Q9LMT1 arabidopsis
8	480	23.8	341	10 Q944K0	Q944K0 arabidopsis
9	474	23.5	242	5 Q62212	Q62212 caenorhabdi
10	408.5	20.2	319	10 Q8S820	Q8S820 mesembryant
11	398.5	19.7	311	10 Q8R3V3	Q8R3V3 arabidopsis
12	381.5	18.9	243	10 Q8S3P1	Q8S3P1 oryza sativ
13	368.5	18.3	420	10 Q8VZD9	Q8VZD9 arabidopsis
14	368	18.2	389	10 Q81773	Q81773 arabidopsis
15	368	18.2	975	5 O15743	O15743 dictyostell
16	366.5	18.2	420	10 Q94AT1	Q94AT1 arabidopsis

17	366.5	18.2	757	4 Q9UPT0	Q9UPT0 homo sapien
18	365	18.1	359	10 Q82469	Q82469 mesembryant
19	365	18.1	766	4 Q8WY54	Q8WY54 homo sapien
20	364.5	18.1	348	10 Q91EW5	Q91EW5 arabidopsis
21	364.5	18.1	371	10 Q8VZD9	Q8VZD9 arabidopsis
22	362	17.9	464	10 Q8VZD9	Q8VZD9 arabidopsis
23	361	17.9	380	10 Q8R3V3	Q8R3V3 arabidopsis
24	359.5	17.8	454	4 Q96PM2	Q96PM2 homo sapien
25	358.5	17.8	361	10 Q9SD02	Q9SD02 arabidopsis
26	353.5	17.5	355	10 Q81716	Q81716 arabidopsis
27	353.5	17.5	362	10 Q8ZP19	Q8ZP19 lotus japon
28	352	17.4	302	10 Q95LAI	Q95LAI arabidopsis
29	352	17.4	302	10 Q95LAI	Q95LAI arabidopsis
30	351	17.4	408	10 Q82200	Q82200 arabidopsis
31	351	17.4	658	10 Q940M2	Q940M2 oryza sativ
32	350	17.3	305	10 Q94ZM4	Q94ZM4 oryza sativ
33	350	17.3	357	10 Q95ZS3	Q95ZS3 arabidopsis
34	341.5	16.9	450	11 Q9WVR7	Q9WVR7 ratu musculi
35	339	16.8	396	10 Q9LPI2	Q9LPI2 arabidopsis
36	338.5	16.8	393	10 Q9XEB8	Q9XEB8 arabidopsis
37	338.5	16.8	390	10 Q9XEB8	Q9XEB8 arabidopsis
38	338.5	16.8	405	10 Q91MK9	Q91MK9 arabidopsis
39	338	16.7	323	11 Q95OE2	Q95OE2 mus musculi
40	338	16.7	326	11 Q95OE3	Q95OE3 mus musculi
41	338	16.7	326	11 Q95OE3	Q95OE3 mus musculi
42	337.5	16.7	380	10 Q82468	Q82468 mesembryant
43	337.5	16.7	380	10 P93006	P93006 arabidopsis
44	336.5	16.7	381	10 Q24078	Q24078 medicago sa
45	336.5	16.7	396	10 Q80871	Q80871 arabidopsis

ALIGNMENTS

RESULT 1
Q9H0C8 PRELIMINARY; PRT; 392 AA.
ID Q9H0C8
AC Q9H0C8
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothesized 42.9 kDa protein (Integrin-linked Kinase-associated serine/threonine phosphatase 2C).
GN DKFZP434J031.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Blum H., Bauersachs S., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Mahendra A., Naruszewicz I., Hannigan G.E.;
RT "Modulation of Integrin signal transduction by ILKAP, a protein
RL phosphatase 2C associating with the Integrin-linked Kinase, ILK1".
RL EMO J. 0:0-0(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL136850; CAB6784.1; -;
DR EMBL: AY024365; AAK07736.1; -;
DR EMBL: BC006576; AAK06576.1; -;
DR HSSP: P35813; 1A60.
DR InterPro: IPR000222; PP2C.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00333; PP2CC; 1.
DR SMART: SM00331; PP2C_SIG; 1.

DR PROSITE; PS01032; PP2C; 1.
 KM Hypothetical protein; Kinase.
 SQ SEQUENCE 392 AA; 42906 MW; AF6ACC98508CBEA3 CRC64;

Query Match 100.0%; Score 2018; DB 4; Length 392;
 Best Local Similarity 100.0%; Pred. No. 4.4e-156;
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRPAAGKEAQKGPILLFDLPPASSTDSGSGGPIILFDLPPASSGDSG 60
 Db 1 MDLFGDLPEPERSPPRPAAGKEAQKGPILLFDLPPASSTDSGSGGPIILFDLPPASSGDSG 60
 QY 61 SLATSSIQWVKTEGKAKKRTSEEEKNGSEELVEKKVCASSVIFGLKGVAAERKGEREE 120
 Db 61 SLATSSIQWVKTEGKAKKRTSEEEKNGSEELVEKKVCASSVIFGLKGVAAERKGEREE 120
 QY 121 MODAHVILNDITEECRPPSSILTRVSYFAVFDGHGIRASKFAAONLHONLIRKFPKGDV 180
 Db 121 MODAHVILNDITEECRPPSSILTRVSYFAVFDGHGIRASKFAAONLHONLIRKFPKGDV 180
 QY 181 ISVEKTVKRCCLDPTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDGRAI 240
 Db 181 ISVEKTVKRCCLDPTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDGRAI 240
 QY 241 LCRVNEESQKHAALSLSKENHPQYEBRMRIQKAGGNVDRGVLEVSRSIGDQGYKR 300
 Db 241 LCRVNEESQKHAALSLSKENHPQYEBRMRIQKAGGNVDRGVLEVSRSIGDQGYKR 300
 QY 301 CGVTSVPDIRRCQLTNDPDRFILACDGLFKVFTPEBAVNFILSCLEDEKIQTRREGKSAAD 360
 Db 301 CGVTSVPDIRRCQLTNDPDRFILACDGLFKVFTPEBAVNFILSCLEDEKIQTRREGKSAAD 360
 QY 361 ARYEACNRLANKAVORGSAADNTVWVVRIGH 392
 Db 361 ARYEACNRLANKAVORGSAADNTVWVVRIGH 392

RESULT 2

QY 09R0F6 PRELIMINARY; PRT; 392 AA.
 AC 09R0F6;
 DT 01-JUN-2002 (T-EMBLrel. 21, Last Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Similar to protein phosphatase 2C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

(1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Strauberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC026953; AAH26953.1;
 SQ SEQUENCE 392 AA; 42774 MW; 8DE1F77DAC9B7176 CRC64;

Query Match 95.2%; Score 1935; DB 11; Length 392;
 Best Local Similarity 95.2%; Pred. No. 2.5e-149;
 Matches 373; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRPAAGKEAQKGPILLFDLPPASSTDSGSGGPIILFDLPPASSGDSG 60
 Db 1 MDLFGDLPEPERSPPRPAAGKEAQKGPILLFDLPPASSTDSGSGGPIILFDLPPASSGDSG 60
 QY 61 SLATSSIQWVKTEGKAKKRTSEEEKNGSEELVEKKVCASSVIFGLKGVAAERKGEREE 120
 Db 61 SLATSSIQWVKTEGKAKKRTSEEEKNGSEELVEKKVCASSVIFGLKGVAAERKGEREE 120
 QY 121 MODAHVILNDITEECRPPSSILTRVSYFAVFDGHGIRASKFAAONLHONLIRKFPKGDV 180
 Db 121 MODAHVILNDITEECRPPSSILTRVSYFAVFDGHGIRASKFAAONLHONLIRKFPKGDV 180

QY 181 ISVEKTVKRCCLDPTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDGRAI 240
 Db 181 ISVEKTVKRCCLDPTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDGRAI 240
 QY 241 LCRVNEESQKHAALSLSKENHPQYEBRMRIQKAGGNVDRGVLEVSRSIGDQGYKR 300
 Db 241 LCRVNEESQKHAALSLSKENHPQYEBRMRIQKAGGNVDRGVLEVSRSIGDQGYKR 300
 QY 301 CGVTSVPDIRRCQLTNDPDRFILACDGLFKVFTPEBAVNFILSCLEDEKIQTRREGKSAAD 360
 Db 301 CGVTSVPDIRRCQLTNDPDRFILACDGLFKVFTPEBAVNFILSCLEDEKIQTRREGKSAAD 360
 QY 361 ARYEACNRLANKAVORGSAADNTVWVVRIGH 392
 Db 361 ARYEACNRLANKAVORGSAADNTVWVVRIGH 392

RESULT 3

QY 09Z1Z6 PRELIMINARY; PRT; 392 AA.
 AC 09Z1Z6;
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
 DE Protein phosphatase 2C.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99074314; PubMed=9857069;
 RA Tong Y., Quilston R., Shen S.H.;
 RT "Cloning and characterization of a novel mammalian PP2C isozyme."
 RL J. Biol. Chem. 273:35282-35290(1998).
 DR EMBL; AF095927; AAC97497.1;
 DR HSSP; P35813; 1A60.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00332; PP2Cg; 1.
 DR SMART; SM00331; PP2C_Sig; 1.
 DR PROSITE; PS01032; PP2C; 1.
 SQ SEQUENCE 392 AA; 42744 MW; 1468FDE0BA60D915 CRC64;

Query Match 95.7%; Score 1931; DB 11; Length 392;
 Best Local Similarity 95.2%; Pred. No. 5.3e-149;
 Matches 373; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRPAAGKEAQKGPILLFDLPPASSTDSGSGGPIILFDLPPASSGDSG 60
 Db 1 MDLFGDLPEPERSPPRPAAGKEAQKGPILLFDLPPASSTDSGSGGPIILFDLPPASSGDSG 60
 QY 61 SLATSSIQWVKTEGKAKKRTSEEEKNGSEELVEKKVCASSVIFGLKGVAAERKGEREE 120
 Db 61 SLATSSIQWVKTEGKAKKRTSEEEKNGSEELVEKKVCASSVIFGLKGVAAERKGEREE 120
 QY 121 MODAHVILNDITEECRPPSSILTRVSYFAVFDGHGIRASKFAAONLHONLIRKFPKGDV 180
 Db 121 MODAHVILNDITEECRPPSSILTRVSYFAVFDGHGIRASKFAAONLHONLIRKFPKGDV 180
 QY 181 ISVEKTVKRCCLDPTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDGRAI 240
 Db 181 ISVEKTVKRCCLDPTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDGRAI 240
 QY 241 LCRVNEESQKHAALSLSKENHPQYEBRMRIQKAGGNVDRGVLEVSRSIGDQGYKR 300
 Db 241 LCRVNEESQKHAALSLSKENHPQYEBRMRIQKAGGNVDRGVLEVSRSIGDQGYKR 300
 QY 301 CGVTSVPDIRRCQLTNDPDRFILACDGLFKVFTPEBAVNFILSCLEDEKIQTRREGKSAAD 360
 Db 301 CGVTSVPDIRRCQLTNDPDRFILACDGLFKVFTPEBAVNFILSCLEDEKIQTRREGKSAAD 360

QY 361 ARYEACNRLANKAVOGSADNTVTVVRIGH 392
DB 361 ARYEACNRLANKAVOGSADNTVTVVRIGH 392

RESULT 4

Q9DC99 PRELIMINARY; PRT; 272 AA.
AC Q9DC99; 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE 0710007A14R1K protein.
GN 0710007A14R1K
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=BRN;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK003007; BAB22508.1; -.
DR HSSP; P35813; IAGQ; 0710007A14R1K.
DR MGD; MGI:1914694; 0710007A14R1K.
DR InterPro; IPR001932; PP2C-1like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 272 AA; 30279 MW; 485F2959D91BA63D CRC64;

Query Match 68.7%; Score 1386; DB 11; Length 272;
Best Local Similarity 97.8%; Pred. No. 7.3e-105;
Matches 266; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 121 MODAVILNDITEECPPSSLTTRVSFAVFDGGIGIRASKFAQNLHONLRFPKGDV 180
DB 1 MODAVILNDITEECPPSSLTTRVSFAVFDGGIGIRASKFAQNLHONLRFPKGDV 180
QY 181 ISVEKTVKRCCLDFTFGTDEEFLKQASSQKPAWMDGSTATCVAVNIIYIANLGDSPAI 240
DB 61 ISVEKTVKRCCLDFTFGTDEEFLKQASSQKPAWMDGSTATCVAVNIIYIANLGDSPAI 120
QY 241 LCRYNESQKHAALSKENHPYOYEERNRLOKAGVNRDGRVGLVEVRSISIGDQYKR 300
DB 121 LCRYNESQKHAALSKENHPYOYEERNRLOKAGVNRDGRVGLVEVRSISIGDQYKR 180
QY 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVTPPEAVNFIISLCEDEKIQTRBEGKSPAD 360
DB 181 CGVTSVPDIRCOLTPNDRFILLACDGLFKVTPPEAVNFIISLCEDEKIQTRBEGKSPAD 240

QY 361 ARYEACNRLANKAVOGSADNTVTVVRIGH 392
DB 241 ARYEACNRLANKAVOGSADNTVTVVRIGH 272

RESULT 5

Q9CS46 PRELIMINARY; PRT; 212 AA.
AC Q9CS46; 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE 0710007A14R1K protein (Fragment).
GN 0710007A14R1K
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMERYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK019158; BAB31574.1; -.
DR HSSP; P35813; IAGQ; 0710007A14R1K.
DR MGD; MGI:1914694; 0710007A14R1K.
DR InterPro; IPR001932; PP2C-1like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR NON_TER 1
FT
SQ SEQUENCE 212 AA; 23615 MW; 133286D628B540D7 CRC64;

Query Match 53.4%; Score 1078; DB 11; Length 212;
Best Local Similarity 98.1%; Pred. No. 6.1e-80;
Matches 208; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 181 ISVEKTVKRCCLDFTFGTDEEFLKQASSQKPAWMDGSTATCVAVNIIYIANLGDSPAI 240
DB 1 ISVEKTVKRCCLDFTFGTDEEFLKQASSQKPAWMDGSTATCVAVNIIYIANLGDSPAI 60
QY 241 LCRYNESQKHAALSKENHPYOYEERNRLOKAGVNRDGRVGLVEVRSISIGDQYKR 300
DB 61 LCRYNESQKHAALSKENHPYOYEERNRLOKAGVNRDGRVGLVEVRSISIGDQYKR 120
QY 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVTPPEAVNFIISLCEDEKIQTRBEGKSPAD 360
DB 121 CGVTSVPDIRCOLTPNDRFILLACDGLFKVTPPEAVNFIISLCEDEKIQTRBEGKSPAD 180
QY 361 ARYEACNRLANKAVOGSADNTVTVVRIGH 392
DB 181 ARYEACNRLANKAVOGSADNTVTVVRIGH 212

RESULT 6

Q920T2 ID Q920T2 PRELIMINARY; PRT; 167 AA.
 AC Q920T2;
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypoetical 18.8 kDa protein (Fragment).
 GN 0710007A1AR1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eulheta; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Stothard P.M., Pilgrim D.;
 RT "Isolation of PP2C sequences using degenerate-oligo PCR."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF117831; AAD17234.1; -.
 DP HSSP; P35813; 1A6Q.
 MGDI: 1914694; 0710007A1AR1K.
 DR InterPro: IPR001932; PP2C-like.
 DR Pfam: PF00481; PP2C; 1.
 DR SMART; SM00332; PP2C; 1.
 KW Hypoetical protein.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 167 AA; 18795 MW; 3A4FC2FEB09DD95B CRC64;
 Query Match 42.4%; Score 856; DB 11; Length 167;
 Best Local Similarity 98.8%; Pred. No. 5.1e-62;
 Matches 165; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 157 IRASKFAQVQLHQLKRPKGVISVEKTVKRCLELTPFHTPEELPKASQKPAWKDG 216
 DB 1 IRASKLAQVQLHQLKRPKGVISVEKTVKRCLELTPFHTPEELPKASQKPAWKDG 60
 QY 217 STATCVLAVNLIYIANLIGDSRAILCRYNESQKHAALSLSKENHPQYEEHMRIOKAGG 276
 DB 61 STATCVLAVNLIYIANLIGDSRAILCRYNESQKHAALSLSKENHPQYEEHMRIOKAGG 120
 QY 277 NVNDRGLVLEVSRSIGDQYKRCGTSVPDIRRCOLTPNDRFILL 323
 DB 121 NVNDRGLVLEVSRSIGDQYKRCGTSVPDIRRCOLTPNDRFILL 167
 RESULT 7
 Q9LMT1 PRELIMINARY; PRT; 341 AA.
 AC Q9LMT1;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE T10F20.4 protein.
 GN T10F20.4.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA.
 RA Sakano H., Liu S.X., Etgu P., Lee J.M., Lenz C., Pham P., Toriumi M.,
 RA Yu G., Han A., Chung M., Goldsmith A., Liu A., Smith A., Vaynsberg M.,
 RA Altali H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
 RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
 RA Nguyen M., Palm C.J., Shin P., Southwick A., Davis R.W., Ecker J.R.,
 RA Federicci N.A., Theologis A.;
 RT "The sequence of BAC T10F20 from Arabidopsis thaliana chromosome 1."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC034107; AA97840.1; -.
 DR HSSP; P35813; 1A6Q.

DR InterPro: IPR001932; PP2C-like.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00332; PP2C; 1.
 DR SMART; SM00331; PP2C; 1.
 SQ SEQUENCE 341 AA; 37367 MW; 6873C0CE82310195 CRC64;
 Query Match 23.8%; Score 481; DB 10; Length 341;
 Best Local Similarity 35.8%; Pred. No. 4.9e-31;
 Matches 119; Conservative 66; Mismatches 107; Indels 40; Gaps 11;
 QY 78 KRRTSEENKNGSELY-----EKVCKASSV-----FLKGVYARKKGEREMODAHYI 127
 DB 24 KAKKSEEVGGGGAVAAGNREAEEDKPSFVSEKKEFLVEDVADKARHTMEDVWVV 83
 QY 128 LNDITECRPPSSLIRVSYFAVFDGHGIRASKFAQVQLHQLKRPKGVISVEKTV 187
 DB 84 LPASLDF--PGL--RCAHFAIYDGHGRLAEPFKKHLHLNLSAGLPRELLD--KYA 138
 QY 188 KRCLDTPFHTPEELPKASQKPAWKDGSTATCVLAVNLIYIANLIGDSRAILCR 243
 DB 139 KKAILEGFRKTDLLQKSVS--GWDGATVACVWILDQKVFVANIIGDAKAVLABSSST 196
 QY 244 -----YNESQKHAALSLSKENHPQYEEHMRIOKAGGV--RDGRVLGVLEVSRSIGDQ 297
 DB 197 NELGNHTEAGNPLKAVLTREHVAIYPOERSRIQKSGVSSNGRLQGVLEVSRAFGDRH 256
 QY 298 YKRCGVTSVPDIRRCOLTPNDRFILLACDGLPKVTPPEAVNFIISLCLEDEKIQTRGKS 357
 DB 257 FKFGVSATPDIIHAFELTERENFMILGCDGLMEVFPSPDAVGFVQLL-----KEG-- 307
 QY 358 AADARYEAACNLRANKAV--QRGSADNVTVWV 388
 DB 308 ---LHVSTVSRRLVKEAVKERRCKDCTAIVI 336
 RESULT 8
 Q944KO PRELIMINARY; PRT; 351 AA.
 AC Q944KO;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE A1518030/T10F20.3.
 GN A1518030/T10F20.3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carlini P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Natrasaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF428352; AAL16282.1; -.
 DR InterPro: IPR001932; PP2C-like.
 DR Pfam; PF00481; PP2C; 1.
 SQ SEQUENCE 351 AA; 38514 MW; AFE224E0E003229 CRC64;
 Query Match 23.8%; Score 480; DB 10; Length 351;
 Best Local Similarity 35.8%; Pred. No. 6.1e-31;
 Matches 119; Conservative 66; Mismatches 107; Indels 40; Gaps 11;
 QY 78 KRRTSEENKNGSELY-----EKVCKASSV-----FLKGVYARKKGEREMODAHYI 127
 DB 34 KAKKSEEVGGGGAVAAGNREAEEDKPSFVSEKKEFLVEDVADKARHTMEDVWVV 93

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QY 128 LMDITECRPSSLTRVSYFAVFGHGCTASKEAFAONHONLIRKPKGVISVEKTV 187
DB 94 LPDASLDP--PGLT--RCAHFAIYDGHGRIALASFAKCHLHNLVLSAGLPRELLDV--RYA 148
QY 188 KRCLLDTPFKHTDEBFLKQASSQKPAWKDGTATCVLAVDNLIYANLGDSPAILCR---- 243
DB 149 KKAILEGFRRTDELLOKSVS--GGMQGAATVAVCWLLDQKRVANAIIGAKKAVLARSTT 206
QY 244 ----YNEESQKHAALSLSKEHNPQYEERNRIQKAGNV--RDGRVLGVLEVSRSIGDQ 297
DB 207 NELGNHTEAGNPJKAIVLTREHKAITYQERSRIOKSGVISNGLQGRLEVSRAFGDRH 266
QY 298 YKRCGVTSVPDIRRCOLTPNDRFILLACDGFXYFTPEEAVNFILSCLDEKIQTRGKS 357
DB 267 FKFGVSGATPDIAHAFETRENFPMILGCDLMEVFGSPDAVGFVQKLT-----KEG-- 317
QY 358 AADARVEACNRLANKAV--ORGADNVTVWV 388
DB 318 ---LHVGTSRLVTKAVKVERCKXNCTAIVI 346

RESULT 9
ID 062212 PRELIMINARY; PRT; 242 AA.
AC 062212:
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE F33A8.6 protein.
GN F33A8.6
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA MEDLINE=94150718; Pubmed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Fothergill J.,
RA Craxton M., Dear S., Dunn R., Eaves L., Fothergill J., Fothergill J.,
RA Gardner A., Green S., Hawkins J., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kistler J., Lalister N., Latreille P.,
RA Lighthill J., Lloyd C., Murray L., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rinken L., Roopra A., Saunders D., Shownkeen R.,
RA Smalton J., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Spoat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38 (1994).
RN (3)
RP SEQUENCE FROM N.A.
RA Mortimore B.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z81525; CAB04260.1; -.
DR EMBL; AL031264; CAB04260.1; JOINED.
DR EMBL; Z81525; CAB04260.1; JOINED.
DR InterPro; IPR000222; P22C.
DR InterPro; IPR001932; P22C-1-like.
DR Pfam; PF00481; P22C.1.
DR SMART; SM00333; P22C.1.
DR PROSITE; PS01032; P22C.1.
SQ SEQUENCE 242 AA; 6286CA6104D34ADC CRC64;

Query Match 23.5%; Score 474; DB 5; Length 242;
Best Local Similarity 40.2%; Pred. No. 11e-30;
Matches 98; Conservative 54; Mismatches 80; Indels 12; Gaps 5;

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QY 82 SEENKSGEELV----EKVCKASVIFGLKGVAEERGEEMODAHVILN--DITEBC 135
DB 3 SOSRRSSDDILINDSDSKPKSRMLICTLAAYCKRGAGADODHILNLPFDLGTB- 61
QY 136 RPPSSLTRVSYFAVFGHGCTASKEAFAONHONLIRKPK-GDVTSVEKTVKRLD 194
DB 62 ---KSFLLRASFPAIFPGHAGPAAHSCOSQKVKERKLKFPDPFTLSLKQFTFS 118
QY 195 FKHTEBFLKQASSQKPAWKDGTATCVLAVDNLIYANLGDSPAILCRYNESQKHAAL 254
DB 119 YKAVDDGFLAIAKQNKPMWDGTTATMILNNVYVANNIDSDRAVARKKEDG--SFAV 177
QY 255 SLSEKNFTQYEERNRIQKAGNVDRGVLEVSRSIGDQYKRCGVTSVPDIRCOL 314
DB 178 CLTVHDDMSHDEMRIOKAGAVVKDGRINGVLEVSRSIGDLPKSGIISTDPLKLT 237
QY 315 TPND 318
DB 238 TRND 241

RESULT 10
ID 088820 PRELIMINARY; PRT; 319 AA.
AC 088820:
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Protein phosphatase 2C.
GN MPC9.
OS Mesembryanthemum crystallinum (common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Aizoaceae; Mesembryanthemum.
OX NCBI_TaxID=3544;
RN (1)
RP SEQUENCE FROM N.A.
RA Miyazaki S., Izumi S., Fukuhara T., Bohnert H.J.;
RT "Plant Protein Phosphatases 2C ? A large protein family serving
RT complex functions."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083482; BAB8944.1; -.
SQ SEQUENCE 319 AA; 34477 MW; 0BD22860334CFB0 CRC64;

Query Match 20.2%; Score 408.5; DB 10; Length 319;
Best Local Similarity 39.6%; Pred. No. 3.5e-25;
Matches 113; Conservative 41; Mismatches 86; Indels 45; Gaps 12;

QY 109 GYVABERKGEREMODAHVILNITECRPSSLTRVSYFAVFGHGCTASKEAFAONH 168
DB 35 GY-ASSPGKSSMEDFETRIDVEG-----EVGLFVFGHGGAAPAAEYVKONLF 85
QY 169 QNLIRKPKGVISVEKTVKRLDTPFKHTDEBFLKQASSQKPAWKD-GSTATCVLAVDN 227
DB 86 SNLI-KHPK--FIS---DTKSAIAEAYTHTDEBFLKSENTON--RDAGSTASTAILVGD 136
QY 228 ILVYANLGDSPAILCRYNESQKHAALSKEHNPQYEERNRIQKAGNV--DGRVL 284
DB 137 RLTVANVGDSPRAVICRGE-----AIVASRDHKPDQSDERORIEDAGGFVMAAGTWRVG 190
QY 285 GVEVSRSIGDQYKRCGVTSVPDIRCOLTPNDRFILLACDGFXYFTPEEAVNFILSCL 344
DB 191 GYLAVSRAFGDKLKKQY-VVADEIQEIVVDSLEFILLADGMDVTVTEAIVTWV---- 246
QY 345 LDEKIQTRGKSADARVEACNRLANKAVYORGADNVTVWV 389
DB 247 -----KPIQDT--EEAAKLMQAHYORGADNVTVVVR 278

RESULT 11
ID 08RXV3 PRELIMINARY; PRT; 311 AA.
AC 08RXV3:

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DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical 33.2 kDa protein.
 GN ATG31750.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Iehida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam C., Lin J.,
 RA Miranda M., Narasaka M., Nguyen N., Palm C.J., Sakurai T., Saito M.,
 RA Seki M., Shimizu F., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 DB "Arabidopsis Full length cDNA clones."
 DB EMBL: AY080658; AAL86334.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 311 AA; 33247 MW; 5E3098E91F116BFD CRC64;
 Query Match 19.7%; Score 398.5; DB 10; Length 311;
 Best Local Similarity 39.3%; Pred. No. 2.2e-24;
 Matches 112; Conservative 40; Mismatches 88; Indels 45; Gaps 12;
 QY 109 GYAERKGEERENDAAVILNDITECRPPSSILTRSYAFVFGHGIRASKAAQNLH 168
 DB 35 GY-ASSPKSSMEDFYETRIDVEG-----EIVGFVFGHGIRASKAAEVKQNL 85
 QY 169 ONLIRPKPGDVIVSEKTVKRCILDTFKHTDEEFLKQASSOKPAWK-GSATCVLAVDN 227
 DB 86 SNLIR-HPK--FIS---DTPLADAVINQDSEFLKSENSON---RAGSTASAILVGD 136
 QY 228 ILVIANTGDSRAILCRYNESQKHAALSKEHNPVYEEEMRIQKAGNVR--DGRVL 284
 DB 137 RLVAANVGDSRAVICRGGN-----ALAVSRDHKPDQSDERQREDAGGFVMAGTWVRG 190
 QY 285 GYLEVSSIGDQYKRCGVTSVPDIRCOLTPNDRFILACDGLFKYFTPEAVNFI 344
 DB 191 GVLAASRAFGDRILKQY--VVADEPIQEEKVSSLEFILLASDGLMDVANSBEAVGM- 248
 QY 345 LEDEKIQTRGKSAADARYEAACNRLANKAVQSGAANVTVMVR 389
 DB 249 IEDP-----EKGAKRLMMEAVIQGSAUNITCVVR 278
 RESULT 12
 ID 0833P1 PRELIMINARY; PRT; 243 AA.
 AC 0833P1;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical 26.7 kDa protein.
 GN 24K23.16.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriocarpaceae; Oryzoideae; Oryza.
 NCBI_TaxId=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV; NIPONBARE;
 RA Park Y.-J., Roscoe N., Ramakrishna W., Samiuel P., Shiloff B.,
 RA Ma J., Jiang Z., Kleinhofs A., Bennett J.;
 RT "Sequence characterization of orthologous regions in the barley and
 rice genomes."
 RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF480497; AAL87187.1; -

KW Hypothetical protein.
 SQ SEQUENCE 243 AA; 26734 MW; 8B481E17F559CSEF CRC64;
 Query Match 18.9%; Score 381.5; DB 10; Length 243;
 Best Local Similarity 37.9%; Pred. No. 3.8e-23;
 Matches 96; Conservative 43; Mismatches 75; Indels 39; Gaps 7;
 QY 145 VSYFAVFDGHCIRASKFAAQNHLIR--KPKPGDVIVSEKTVKRCILDTFKHTDEEF 202
 DB 17 IGLFVFDGHCIRASKFAAQNHLIR--KPKPGDVIVSEKTVKRCILDTFKHTDEEF 68
 QY 203 LKQASSQKPAWKDGSATATCVLAVNITLYANLSDSRALICRYNEESQKHAALSKEHNP 262
 DB 69 LKQASSQKPAWKDGSATATCVLAVNITLYANLSDSRALICRYNEESQKHAALSKEHNP 119
 QY 263 TOYEEMRIQKAGNVR--DGRVLGVLEYSRISGQYRCGVTSVPDIRCOLTPNDR 319
 DB 120 DQTEQRLEDDAGFVMAAGTWRVGVLAASRAFGDRILKQYVVD--PEIRREVYDHSLE 178
 QY 320 FILACDGLFKYFTPEAVNFIISLCEDEKIQTRGKSAADARYEAACNRLANKAVQSGS 379
 DB 179 FILACDGLMDVITNEAVDMTRSHDPE-----AAKLQDAVKRES 222
 QY 380 ADVNVTVMVRIGH 392
 DB 223 SDNITCVVRFLH 235
 RESULT 13
 ID 08VZD9 PRELIMINARY; PRT; 420 AA.
 AC 08VZD9;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE ATG533140/MFH8.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Iehida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narasaka M., Saito M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Saito M.,
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones."
 RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY065026; AAL5766.1; -
 DR InterPro: IPR000222; PP2C.
 DR Pfam: PF00481; PP2C-1.
 DR SMART: SM00332; PP2C-1.
 DR SMART: SM00331; PP2C-SIG. 1.
 DR PROSITE: PS01032; PP2C; UNKNOWN 1.
 SQ SEQUENCE 420 AA; 45752 MW; 2DF696DD75BF9058 CRC64;
 Query Match 18.3%; Score 368.5; DB 10; Length 420;
 Best Local Similarity 32.8%; Pred. No. 9.5e-22;
 Matches 112; Conservative 60; Mismatches 108; Indels 61; Gaps 13;
 QY 64 TSISQVKTGKGAKKTSSEKNGSEELVEKKVCASSVIFGLK-----GYAERK 115
 DB 58 TSAMKVVDT-----SAGEKRIILVMDPEKVDGVIYGGWKDDGSLSGYCSFR- 108
 QY 116 GEREEMQDAVILNDITECRPPSSILTRSYAFVFGHGIRASKFAAQNHLIRK 175
 DB 109 GKSTMEFDYDIKASTIEG-----QAVCMGIFDGHGGSRAAEYLKXHLNLM-KH 159

QY 176 PKGVISVEKTVKRCCLDTFKHTDEEFLKQSSQKPAWK-DGSTATCVLAADNIIYANL 234
 DB 160 P0-----FLDTTKALAEITKQDYAFLE-----SEKDYTRDGGSTASAAVLGNHLYANV 211
 QY 235 GDSRAILCRYNESQKHAALSKEHNPTQYEEEMRIQKAGNVN--DGRVLGVLEVR 291
 DB 212 GDSRTIV-----SKGAKIALSDDHKPRSDERRKIESAGVIMAGTWRGVLAWSR 265
 QY 232 SIGDQYKRCGVTSVPDIRRCQLTTPNDRFILLACDGLPKVFTPEEAVNFIISCLEDEKIQ 351
 DB 266 ALGNRMKQF-VVAEPIQDLEIDHEALVLAISDGLMDVVPNEADV--ALAQSEEP-- 320
 QY 352 TREGSADARVEACNRLANKAVORGSAADNTVAVVRIGH 392
 DB 321 -----EAAARKLDTAFSGSADNITCIYVKFRH 349

RESULT 14

PRELIMINARY; PRT; 389 AA.

081773; 081773;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical 42.6 kDa protein.
 GN F28M20.60 OR ATAG31750
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Euphorbia II; Brassicales; Brassicaceae; Arabidopsis.
 OK NCBI_TaxId3702;
 RN [1]
 RA SEQUENCE FROM N.A.
 RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Hohnselt J.,
 RA Wewes H.W., Mayer K.F.X., Schueler C., Beyan M.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RA SEQUENCE FROM N.A.
 RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Wewes H.W.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RA SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031004; CAA19748.1; -
 DR HSSP; P35813; IAG0.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PF00481; PP2C_1.
 DR SMART; SM00332; PP2C; 1.
 DR SMART; SM00331; PP2C SIG; 1.
 DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
 DR PROSITE; PS01032; PP2C_1.
 KW Hypothetical protein.
 SQ SEQUENCE 389 AA; 42562 MW; A7C4C39764ECLDEA CRC64;

Query Match 18.2%; Score 368; DB 10; Length 389;

Best Local Similarity 33.7%; Pred. No. 9.3e-22;

Matches 114; Conservative 40; Mismatches 86; Indels 98; Gaps 14;
 QY 109 GYVAERGEREEMQDAHVILNDITEECRPSSLLITRVSYAVFVGGIRASKFAAQNLIH 168
 DB 60 GY-ASSPKRSMEDDEYERIGVGG-----EIVGLFGVFDGIGARRAAEYKQLF 110
 QY 169 QNLIRKPKGDVISEKTVKRCCLDTFKHTDEEFLKQSSQKPAWKD-GSTATCVLAADN 227
 DB 111 SNLIR-HPK--FTS---DTTAAIADAVYQGTSEFLKSENSQN---RDAGSTASTAIVGD 161
 QY 228 ILVIANLGDRAILCRYNESQKHAALSKEHNPTQYEEEMRIQKAGNVN--DGRVL 284

DB 162 RLIVANVGSRVITCRGN-----AIAVRKHDPQSDERKQIEDAGGVMMAGTWRVG 215
 QY 285 GVLEVSRSITGGQYKRCGVTSVPDIR-----SEKDYTRDGGSTASAAVLGNHLYANV 310
 DB 216 GVLAASRAFGPRLKQF-VVADEPIQDLEIDHEALVLAISDGLMDVVPNEADV--ALAQSEEP-- 320
 QY 311 -----RCQLTTPNDR-----FILLACDGLPKVFTPEEAVNFIISCLEDEKIQ 351
 DB 275 NGLTQNFRLRSITISNGFQEKVDSLEFLIILASDGLMDVVPNEADV--ALAQSEEP-- 330
 QY 352 TREGSADARVEACNRLANKAVORGSAADNTVAVVR 389
 DB 331 -----EAGARKLMMEAVYORGSAADNITCVVR 356

RESULT 15

PRELIMINARY; PRT; 975 AA.

015743; 015743;
 AC 015743;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Spalten.
 GN SPVA.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OK NCBI_TaxId44689;
 RN [1]
 RA SEQUENCE FROM N.A.
 RA STRAIN=AX3;
 RC MEDLINE=98252837; PubMed=9585512;
 RX Aubry L., Firtel R.A.;
 RT "Spalten, a protein containing Galpha-protein-like and PP2C domains,
 RT is essential for cell-type differentiation in Dictyostelium."
 RL Genes Dev. 12:1525-1538 (1998).
 DR EMBL; AF019985; AAB70844.1; -
 DR HSSP; P35813; IAG0.
 DR InterPro; IPR001019; Gproteinh_alpha.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PF00503; G-alpha_1.
 DR Pfam; PF00481; PP2C_1.
 DR PRODOM; PD000281; Gproteinh_alpha; 1.
 DR SMART; SM00275; G-alpha; 1.
 DR SMART; SM00332; PP2C; 1.
 DR SMART; SM00331; PP2C SIG; 1.
 DR PROSITE; PS01032; PP2C_1.
 SQ SEQUENCE 975 AA; 109016 MW; BBB322F5026D2A4F CRC64;

Query Match 18.2%; Score 368; DB 5; Length 975;

Best Local Similarity 28.1%; Pred. No. 3.5e-21;

Matches 118; Conservative 56; Mismatches 152; Indels 80; Gaps 17;
 QY 8 PEPEPSPPPAAGKNAQKQGLFDFDLPPASSTDSGSGGFLFDFDLPPASSGDSGLATIS 67
 DB 620 PKPPEKPKPT--KEPKKPVK--SKRPKE-----PKPIKPKSKPKPKPK 661
 QY 68 QNVKTEGKANKRTS-----EEKNGSEEL--VEKKVCKASSVIFGLKGVAKRGE 117
 DB 662 KEPKTKPKPKKRTSKYDGAESKKNKGAUSCNGGVSKILLEG--FG-----SLQGR 713
 QY 118 REEMQDAHVILNDITEECR--PPSSLLITRVSYAVFVGGIRASKFAAQNLIHQLI-- 172
 DB 714 RKNMDDTVILNINMGAVYVNGPCKDI--PISYAVVYHGCGTETSTLEPTVHNCVNS 771
 QY 173 RKFPKGDVISEKTVKRCCLDTFKHTDEEFLKQSSQKPAWKD-GSTATCVLAADNIIYIA 232
 DB 772 QSFPRGCD-----YEAQFRDAVAEADDIIEKE-----KSGSTGVSAALVGNKLYTA 818
 QY 233 NIGDSRAILCRYNESQKHAALSKEHNPTQYEEEMRIQKAGNVN-DGRVL 287
 DB 819 NVGDSIEIVLARAQANAPKPGPYEIVLSTYKHLASDDQEKRRVTDGLGIIIFNRLFSL 876

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2003, 09:35:03 ; Search time 39 Seconds

(without alignments)
1339.340 Million cell updates/sec

Title: US-09-935-124a-2

Perfect score: 1 MDLFDLPBPRSPRPAK.....KAVRGSLDNTVTVVRIGH 392

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SID82/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2018	100.0	392	22	AA828791
2	2018	100.0	392	22	AB805726
3	2018	100.0	421	22	AB812317
4	2018	100.0	421	22	AA40555
5	2018	100.0	441	22	AAU23566
6	2018	100.0	446	22	AAU22933
7	2015	99.9	392	22	AA892585
8	2014	99.8	392	22	AA838769
9	1457.5	72.2	378	22	AB809937
10	928	46.0	221	22	AB809936

11	533.5	26.4	211	22	AB807619	Novel human diapo
12	447.5	22.2	138	22	AAU23252	Novel human enzyme
13	431.5	21.4	295	21	AA818068	Arabidopsis thalia
14	431.5	21.4	305	21	AA818067	Arabidopsis thalia
15	404	20.0	86	21	AA803424	Human secreted pro
16	391.5	19.4	219	21	AA818068	Arabidopsis thalia
17	370.5	18.4	353	23	AB875579	Physcomitrella pat
18	370.5	18.4	354	23	AA869997	Arabidopsis thalia
19	366.5	18.2	360	21	AA816902	Arabidopsis thalia
20	366.5	18.2	383	21	AA818039	Arabidopsis thalia
21	366.5	18.2	420	21	AA818039	Arabidopsis thalia
22	366.5	18.2	420	21	AB808328	Human-derived proc
23	364	18.0	358	21	AA818041	Arabidopsis thalia
24	364	18.0	358	21	AA818041	Arabidopsis thalia
25	364	18.0	359	21	AA818040	Arabidopsis thalia
26	364	18.0	359	21	AA818040	Arabidopsis thalia
27	363	18.0	309	21	AA806998	Arabidopsis thalia
28	358.5	17.8	361	23	AB826620	Herbicidally activ
29	353.5	17.5	355	21	AA83887	Arabidopsis thalia
30	353.5	17.5	438	22	AA82980	Trichoderma reesei
31	353.5	17.5	438	22	AA815376	Trichoderma reesei
32	352.5	17.5	434	22	AA801344	Arabidopsis thalia
33	352	17.4	276	21	AA816903	Arabidopsis thalia
34	350	17.3	357	21	AA832327	Arabidopsis thalia
35	349	17.3	329	21	AA832328	Arabidopsis thalia
36	346	17.1	327	21	AA83888	Arabidopsis thalia
37	345.5	17.1	434	22	AA801348	Arabidopsis thalia
38	341.5	16.9	326	21	AA816904	Arabidopsis thalia
39	341	16.9	322	21	AA843239	Arabidopsis thalia
40	339	16.8	320	21	AA843889	Arabidopsis thalia
41	338.5	16.8	383	21	AA809824	Arabidopsis thalia
42	337.8	16.7	382	23	AB857083	Mouse leishmania co
43	337.5	16.7	387	21	AA879863	A. thaliana enyrio
44	336	16.7	367	22	AB862019	Drosophila melanog
45	336	16.7	382	23	AB861491	Human NF-kB activa

ALIGNMENTS

RESULT 1	AA828791	standard; Protein; 392 AA.
ID	AA828791	
AC	AA828791	
DT	13-FEB-2001	(first entry)
XX		Human hydrolase-like molecule 2 protein.
DB		Hydrolase-like molecule; human; cell proliferation disorder;
XX		autoimmune; cancer; AIDS; acquired immune deficiency syndrome.
KW		Homo sapiens.
OS		
PN	US6132964-A.	
XX		
PD	17-OCT-2000.	
XX		
FE	06-FEB-1998;	98US-0013881.
XX		
PR	06-FEB-1998;	98US-0013881.
XX		
PA	(INCY-) INCYTE PHARM INC.	
XX		
PI	Bandman O, Hillman JL, Guegler KJ, Shah P, Lal P, Corley NC;	
XX	WPI, 2001-006133/01.	
DR	N-PSDB; AAC60224.	
XX		
PT	New human hydrolase-like molecules (HHLMs) and polynucleotides encoding	
PT	the HHLMs, useful for diagnosing, treating or preventing cell	
PT	proliferation (e.g. bone cancer) or autoimmune disorders(e.g. AIDS or	

XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX
PS

XX Example 2; SEQ ID NO 5486; 10078bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA38642-AA42213) with neurotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX Sequence 421 AA:

Query Match 100.0%; Score 2018; DB 22; Length 421;

Best Local Similarity 100.0%; Pred. No. 6.4e-187;

Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 30 MDLFGFLPPEPSPRAAGKEAKGKGLLFDLPPASTSGSGGPLLFDLPPASSGDSG 89
QY 61 STATISQWKTGEGKAKRTSEENKSGSELYEKVCKASSYTFGLKGVYERKGERE 120
DB 90 STATISQWKTGEGKAKRTSEENKSGSELYEKVCKASSYTFGLKGVYERKGERE 149
QY 121 MODAHVILNDITEECRPPSSLITRVSYFAVFDHGIRASKFAAQMHLNLRKPKGDV 180
DB 150 MODAHVILNDITEECRPPSSLITRVSYFAVFDHGIRASKFAAQMHLNLRKPKGDV 209
QY 181 ISEKTVKRCCLDTPFHTDEEFLKQASSQKPAWKDSTATCVLAVNNIYIANLGDSRAI 240
DB 210 ISEKTVKRCCLDTPFHTDEEFLKQASSQKPAWKDSTATCVLAVNNIYIANLGDSRAI 269
QY 241 LCRYNEESQKHAALSLSEKHNPTQYERMRIOKAGNVADGRVLGVLEVSRSIGDSQYR 300
DB 270 LCRYNEESQKHAALSLSEKHNPTQYERMRIOKAGNVADGRVLGVLEVSRSIGDSQYR 329
QY 301 CGVTSPDIRRCQLTENDRFFILLACDGLFKVFTPEBAVNFILSCLEDEKIQTRREGKSAAD 360
DB 330 CGVTSPDIRRCQLTENDRFFILLACDGLFKVFTPEBAVNFILSCLEDEKIQTRREGKSAAD 389
QY 361 ARYEAAACNRLANKAVORGSAADNTVWVRIGH 392.
DB 390 ARYEAAACNRLANKAVORGSAADNTVWVRIGH 421

RESULT 5

AAU23566

ID AAU23566 standard; Protein; 441 AA.

AC AAU23566;

DT 17-DEC-2001 (first entry)

XX Novel human enzyme polypeptide #652.

XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;

KM nephrotropic; anticoagulant.

OS Homo sapiens.

PN WO200155301-A2.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US01239.

PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226881.

PR 22-AUG-2000; 2000US-0226868.

PR 23-AUG-2000; 2000US-0227182.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0228287.

PR 01-SEP-2000; 2000US-0229344.

PR 01-SEP-2000; 2000US-0229345.

PR 05-SEP-2000; 2000US-0229509.

PR 05-SEP-2000; 2000US-0229512.

PR 06-SEP-2000; 2000US-0230437.

PR 06-SEP-2000; 2000US-0230438.

PR 08-SEP-2000; 2000US-0231242.

PR 08-SEP-2000; 2000US-0231243.

PR 08-SEP-2000; 2000US-0231244.

PR 08-SEP-2000; 2000US-0231413.

PR 08-SEP-2000; 2000US-0231414.

PR 08-SEP-2000; 2000US-0232080.

PR 08-SEP-2000; 2000US-0232081.

PR 12-SEP-2000; 2000US-0231968.

PR 14-SEP-2000; 2000US-0233397.

PR 14-SEP-2000; 2000US-0233398.

PR 14-SEP-2000; 2000US-0233399.

PR 14-SEP-2000; 2000US-0233400.

PR 14-SEP-2000; 2000US-0233401.

PR 14-SEP-2000; 2000US-0233063.

PR 14-SEP-2000; 2000US-0233064.

PR 14-SEP-2000; 2000US-0233065.

PR 21-SEP-2000; 2000US-0234223.

PR 21-SEP-2000; 2000US-0234274.

PR 25-SEP-2000; 2000US-0234997.

[illegible]

XX	PA	(HUMA-) HUMAN GENOME SCI INC.
XX	PI	Rosen CA, Barash SC, Ruben SM;
XX	DR	WPI, 2001-465566/50.
XX	DR	N-PSDB; AAS41436.
XX	PT	Novel polypeptides and polynucleotides useful for diagnosing,
XX	PT	preventing, treating neural, immune system, muscular, reproductive,
XX	PT	pulmonary, cardiovascular, renal, proliferative disorders and cancerous
XX	PT	diseases
XX	XX	Claim 11; SEQ ID NO 1562; 1180bp; English.
XX	XX	The present invention relates to the isolation of novel human enzyme
XX	XX	polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
XX	XX	encoding them. The enzyme polypeptides of the invention may comprise the
XX	XX	functional classes of oxidoreductases, transferases, hydrolases, lyases,
XX	XX	isomerases or ligases. The sequences of the invention are useful in the
XX	XX	diagnosis, treatment, prevention and/or prognosis of a wide range of
XX	XX	disorders including hyperproliferative disorders (e.g. cancer),
XX	XX	immunodeficiency disorders (e.g. AIDS) autoimmune disorders
XX	XX	(e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
XX	XX	metabolic disorders (e.g. phenylketonuria), inflammatory disorders
XX	XX	(e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
XX	XX	blood-related disorders (e.g. haemophilia), reproductive disorders
XX	XX	(e.g. infertility) and infectious disorders (e.g. Influenza). The
XX	XX	polynucleotides of the invention can also be used in gene therapy.
XX	XX	AU229315-AU232814 represent the novel human enzyme polypeptides of the
XX	XX	invention.
XX	XX	Note: The sequence data for this patent did not form part of the printed
XX	XX	specification, but was obtained in electronic format directly from WIFO
XX	XX	at ftp.wifo.at/pub/published_pct_sequences.
XX	XX	Sequence 441 AA;
XX	XX	
XX	XX	Query Match 100.0%; Score 2018; DB 22; Length 441;
XX	XX	Best Local Similarity 100.0%; Pred. No. 6.9e-187; Indels 0; Gaps 0;
XX	XX	Matches 392; Conservative 0; Mismatches 0;
QY	1	MDLFGDLPPEERSPPRAAGKEAKOGKPLLPDLPASSSTGSGGCPPLFDLPASSGDSG 60
DB	50	MDLFGDLPPEERSPPRAAGKEAKOGKPLLPDLPASSSTGSGGCPPLFDLPASSGDSG 109
QY	61	SLATSIQWKTGTGKAKAKTISEEKSGSELVEKKVCASSVIFGLKGYVARKERE 120
DB	110	SLATSIQWKTGTGKAKAKTISEEKSGSELVEKKVCASSVIFGLKGYVARKERE 169
QY	121	MODAHVILNDITECHPSSLITRVSYFAVFDHGGIRSKSKPAQNLHONLIRPKGCV 180
DB	170	MODAHVILNDITECHPSSLITRVSYFAVFDHGGIRSKSKPAQNLHONLIRPKGCV 229
QY	181	ISVKTYKRCCLDTPGHDEEFLKQASOKPAKQDSTTCVLAVNDILVYANLGSRAI 240
DB	230	ISVKTYKRCCLDTPGHDEEFLKQASOKPAKQDSTTCVLAVNDILVYANLGSRAI 289
QY	241	LCRNESQGHALSLSKENHPTQYERRMILQAGGNVDRGVGULEVSRSLGDOYR 300
DB	290	LCRNESQGHALSLSKENHPTQYERRMILQAGGNVDRGVGULEVSRSLGDOYR 349
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QY	361	ARYEACNRLANKAVORGADNVTVVVRIGH 392
DB	410	ARYEACNRLANKAVORGADNVTVVVRIGH 441
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XX	XX	AU22933 standard; Protein: 446 AA
XX	XX	ID AU22933

XX AAU22933;
AC
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human enzyme polypeptide #19.
XX
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX
OS Homo sapiens.
XX
PN WO200155301-A2.
PD
02-AUG-2001.
17-JAN-2001; 2001WO-US01239.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
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PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
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PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
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PR 05-SEP-2000; 2000US-0229509.
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PR 17-NOV-2000; 2000US-0249209.
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PR 17-NOV-2000; 2000US-0249211.
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PR 17-NOV-2000; 2000US-0249216.
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PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.

PR	01-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251859.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0239678.
XX	(HUMA-) HUMAN GENOME SCI INC.	
PA	Rosen CA, Barash SC, Ruben SM;	
PL	WPI; 2001-465566/50.	
DR	N-PSDB; AAS40803.	
XX	Newel polypeptides and polynucleotides useful for diagnosing,	
XX	preventing, treating neural, immune system, muscular, reproductive,	
XX	pulmonary, cardiovascular, renal, proliferative disorders and cancerous	
PT	diseases -	
XX	Claim 11; SEQ ID NO 929; 1180bp; English.	
XX	The present invention relates to the isolation of novel human enzyme	
CC	polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences	
CC	encoding them. The enzyme polypeptides of the invention may comprise the	
CC	functional classes of oxidoreductases, transferases, hydrolases, lyases,	
CC	isomerases or ligases. The sequences of the invention are useful in the	
CC	diagnosis, treatment, prevention and/or prognosis of a wide range of	
CC	disorders, including hyperproliferative disorders (e.g. cancer),	
CC	immunodeficiency disorders (e.g. AIDS), autoimmune disorders (disease),	
CC	(e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),	
CC	metabolic disorders (e.g. phenylketonuria), inflammatory disorders	
CC	(e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),	
CC	blood-related disorders (e.g. haemophilia), reproductive disorders	
CC	(e.g. infertility) and infectious disorders (e.g. influenza). The	
CC	polynucleotide of the invention can also be used in gene therapy.	
CC	AAM22915-AAM23814 represent the novel human enzyme polypeptides of the	
CC	invention.	
CC	Note: The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences.	
XX	Sequence 446 AA;	
S0		
OY	1 MDLFGDLPPEPSPRPAPAGKAGKGPLFDDLPASSSTDSGSGPLFPDLPPASSGSG 60	
D0	55 MDLFGDLPPEPSPRPAPAGKAGKGPLFDDLPASSSTDSGSGPLFPDLPPASSGSG 114	
OY	61 SLATSLISOMVTEBKGAKRTKEEBEKGSEELVEKKVKCKASVIFGLKGVYERKGEFE 120	
D0	115 SLATSLISOMVTEBKGAKRTKEEBEKGSEELVEKKVKCKASVIFGLKGVYERKGEFE 174	
OY	121 MODAVIYLNDITBECRPPSSILTRYSIVAFVFPGHGIGIPASKFAONLHQLIRPKPKDV 180	
D0	175 MODAVIYLNDITBECRPPSSILTRYSIVAFVFPGHGIGIPASKFAONLHQLIRPKPKDV 234	
OY	181 ISYEKTVRCLLDTPFKCTIDEPFLKQASQSKPMWKDGSTATCTVLAVNLIYINLGDSRAI 240	
D0	235 ISYEKTVRCLLDTPFKCTIDEPFLKQASQSKPMWKDGSTATCTVLAVNLIYINLGDSRAI 294	
OY	241 LCRKYNEESOKIAALSLSEKHNPFOYEEERNRIQACAGNNRDGRVLGLEVSRSIGDGQYKR 300	
D0	295 LCRKYNEESOKIAALSLSEKHNPFOYEEERNRIQACAGNNRDGRVLGLEVSRSIGDGQYKR 354	

Oy 301 CGCTGVPPIRRCQCTPDRILLACCGGFKFTEFEAVNFIILSCLEDEXIOTRECKSAD 367
Db 355 CCGTGVDPDIRRCQCTPDRILLACCGGFKFTEFEAVNFIILSCLEDEXIOTRECKSAD 414

Oy 361 ABEAACACRLANKRVAGSDNVNTVMVRIH 392
Db 415 ABEAACACRLANKRVAGSDNVNTVMVRIH 446

RESULT 7
AAB92585
ID AAB92585 standard; Protein; 392 AA.
XX
XX AAB92585;
AC
XX 26-JUN-2001 (first entry)
DT
XX Human protein sequence SEQ ID NO:10816.
DE
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
KW
XX Homo sapiens.
OS
XX EPI074617-A2.
PV
XX EPI074617-A2.
PD
XX 07-FEB-2001.
PF
XX 28-JUL-2000; 2000EP-0116126.
PR
XX 23-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 03-JUN-2000; 2000JP-0241899.
PX
PX (HELI-) HELIX RES INST.
PA
Oca T, Isegai T, Nishikawa T, Hayashi K, Saio K, Yamamoto J,
Pl Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
Dr WPI; 2001-318749/34.

Pt Primer sets for synthesizing polynucleotides, particularly the 5602
Pt full-length cDNAs defined in the specification, and for the detection
Pt and/or diagnosis of the abnormality of the proteins encoded by the
Pt full-length cDNAs -
XX

Claim 8; SEQ ID 10816; 2537bp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the combination
CC of oligonucleotide comprises at least 15 nucleotides and the combination
CC of the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH51893 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB93683 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
XX of the present invention.
XX
XX Sequence 392 AA;

Query Match 99.9%; Score 2015; DB 22; Length 392;
 Best Local Similarity 99.7%; Pred. No. 1, 1e-186;
 Matches 391; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRAAGKEAOKGPLLFDLPASTDSGSGPLLFDLPASSGDSG 60
 DB 1 MDLFGDLPEPERSPPRAAGKEAOKGPLLFDLPASTDSGSGPLLFDLPASSGDSG 60
 QY 61 SLATSIQWVKTGKAKRTSEEEKNGSEELVEKVCASSVIFGLKGYAERKGEREE 120
 DB 61 SLATSIQWVKTGKAKRTSEEEKNGSEELVEKVCASSVIFGLKGYAERKGEREE 120
 QY 121 MODAHVILNDITEECPSPSLITRVSYFAVFDGSGIRASKFAAQNHLONLIRKPKGDV 180
 DB 121 MODAHVILNDITEECPSPSLITRVSYFAVFDGSGIRASKFAAQNHLONLIRKPKGDV 180
 QY 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAKMGSTATCVLAVNLIYIANLGDSPRAI 240
 DB 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAKMGSTATCVLAVNLIYIANLGDSPRAI 240
 QY 241 LCRVNEESQKHAALSLSKEHNPTOYEEHRMIOKAGGNVDRGLGVLEVSRSIGDGOYKR 300
 DB 241 LCRVNEESQKHAALSLSKEHNPTOYEEHRMIOKAGGNVDRGLGVLEVSRSIGDGOYKR 300
 QY 301 CGVTSVPDIRRCQLTNPDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTEEGKSAAD 360
 DB 301 CGVTSVPDIRRCQLTNPDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTEEGKSAAD 360
 QY 361 ARYEACNRLANKAVORGSAADNTVMVVRIGH 392
 DB 361 ARYEACNRLANKAVORGSAADNTVMVVRIGH 392

RESULT 8

AAM38769 standard; Protein; 392 AA.

QY 22-OCT-2001 (first entry)
 DB Human polypeptide SEQ ID NO 1914.
 QY Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 peripheral nervous system; neuropathy; central nervous system; CNS;
 Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemoclastic;
 chemokine; chromolytic; drug screening; arthritis; inflammation;
 Leukaemia.
 QY Homo sapiens.
 DB WO200153312-A1.
 QY 26-JUL-2001.
 DB 26-DEC-2000; 2000WC-US34263.
 QY 21-JAN-2000; 2000US-0488725.
 DB 25-APR-2000; 2000US-0552317.
 QY 09-JUL-2000; 2000US-0598042.
 DB 19-JUL-2000; 2000US-0620312.
 QY 03-AUG-2000; 2000US-0653450.
 DB 14-SEP-2000; 2000US-0662191.
 QY 19-OCT-2000; 2000US-0693036.
 DB 29-NOV-2000; 2000US-0727344.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.
 DR N-PSDB; AA157925.

PT Novel nucleic acids and polypeptides, useful for treating disorders
 such as central nervous system injuries -

Example 3; SEQ ID NO 1914; 10078pp; English.

CC The invention relates to human nucleic acids (AA157928-AA161369) and
 CC the encoded polypeptides (AAM38642-AA442213) with nocotropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC activation/inhibition activity, chemotactic/chemokine activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: the sequence data for this patent did not form part of the printed
 CC specification.

Sequence 392 AA:

Query Match 99.8%; Score 2014; DB 22; Length 392;
 Best Local Similarity 99.7%; Pred. No. 1, 4e-186;
 Matches 391; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRAAGKEAOKGPLLFDLPASTDSGSGPLLFDLPASSGDSG 60
 DB 1 MDLFGDLPEPERSPPRAAGKEAOKGPLLFDLPASTDSGSGPLLFDLPASSGDSG 60
 QY 61 SLATSIQWVKTGKAKRTSEEEKNGSEELVEKVCASSVIFGLKGYAERKGEREE 120
 DB 61 SLATSIQWVKTGKAKRTSEEEKNGSEELVEKVCASSVIFGLKGYAERKGEREE 120
 QY 121 MODAHVILNDITEECPSPSLITRVSYFAVFDGSGIRASKFAAQNHLONLIRKPKGDV 180
 DB 121 MODAHVILNDITEECPSPSLITRVSYFAVFDGSGIRASKFAAQNHLONLIRKPKGDV 180
 QY 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAKMGSTATCVLAVNLIYIANLGDSPRAI 240
 DB 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAKMGSTATCVLAVNLIYIANLGDSPRAI 240
 QY 241 LCRVNEESQKHAALSLSKEHNPTOYEEHRMIOKAGGNVDRGLGVLEVSRSIGDGOYKR 300
 DB 241 LCRVNEESQKHAALSLSKEHNPTOYEEHRMIOKAGGNVDRGLGVLEVSRSIGDGOYKR 300
 QY 301 CGVTSVPDIRRCQLTNPDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTEEGKSAAD 360
 DB 301 CGVTSVPDIRRCQLTNPDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTEEGKSAAD 360
 QY 361 ARYEACNRLANKAVORGSAADNTVMVVRIGH 392
 DB 361 ARYEACNRLANKAVORGSAADNTVMVVRIGH 392

RESULT 9

ABG09937 standard; Protein; 378 AA.

ABG09937;

13-FEB-2002 (first entry)

Novel human diagnostic protein #9928.

Human; chromosome mapping; gene mapping; gene therapy; forensic;
 Food supplement; medical imaging; diagnostic; genetic disorder.


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XX OS Homo sapiens.
XX OS
XX PN WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX PF 30-MAR-2001; 2001WO-US08631.
XX
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Drmanac RT, Liu C, Tang YT;
XX
XX DR WPI: 2001-639362/73.
XX DR N-PSDB; AAS74124.
XX
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX
XX PS Claim 20; SEQ ID No 40296; 103pp; English.
XX
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful for medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human
XX CC diagnostic amino acid sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 378 AA;
XX
XX Query Match 72.2%; Score 1457.5; DB 22; Length 378;
XX Best Local Similarity 77.9%; Pred. No. 1,3e-132;
XX Matches 303; Conservative 13; Mismatches 46; Indels 27; Gaps 6;
XX
OY 20 KEAOKPPLFDLPPASSTDSGSGPPLFDLPPASSGDSGLATISISQWKEGKAKR 79
Db 1 KEAOKPPLFDLPPASSTPSA-----VAALGTTPSPVLWFLQTRRSKIWR 49
OY 80 KTSBEKNGSEELVKKYCK-----ASSVIFLKUYVERGESEEMODAHVI 127
Db 50 SLIYOSKVAEPWCHERQOKADRFGLGRGVSPASSYVFLKUYVERGESEEMODAHVI 109
OY 128 LNDITECRPPSLITRVSYPAVFDGCGIRAKPFAOKLHONLRKPKDVSVEKTY 187
Db 110 LNDITECRPPSLITRVSYPAVFDGCGIRAKPFAOKLHONLRKPKDVSVEKTY 169
OY 188 KRCLLTPFHTEDEEFLKQASSOKPAMWDSGTATCVAVNIIYINLSDSAIICRYNE 247
Db 170 KRCLLTPFHTEDEEFLKQASSOKPAMWDSGTATCVAVNIIYINLSDSAIICRYNE 229
OY 248 SOKHAALSLSKHEHNTQYERMRIOXAGNVRCGRVLGLVLEYSRISGGQYKRCGV-TSV 306
Db 230 SOKHAALSLSKHEHNTQYERMRIOXAGNVRCGRVLGLVLEYSRISGGQYKRCGCHLCA 289

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OY 307 PDIRCOLTPNDRFILL-ACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSADARYEA 365
Db 230 PFSRCQLTNPDRFILLWPCDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSADARYEA 349
OY 366 A-CNRLANKAVRGCS-ADNVTVMVVRIGH 392
Db 350 SPATRLANKAVNAGARPDMVTVMVVRIGH 378

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RESULT 10

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ABG09936
XX ID ABG09936 standard; Protein; 221 AA.
XX AC
XX ABG09936;
XX DT 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #9927.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Drmanac RT, Liu C, Tang YT;
XX
XX DR WPI: 2001-639362/73.
XX DR N-PSDB; AAS74123.
XX
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX
XX PS Claim 20; SEQ ID No 40295; 103pp; English.
XX
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful for medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human
XX CC diagnostic amino acid sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SO Sequence 221 AA;
XX
XX Query Match 46.0%; Score 928; DB 22; Length 221;

```

Best Local Similarity 95.8%; Pred. No. 1.5e-81;
Matches 184; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 MDLFGDPEPERSPRPAKGEAKGGLFPDLPASSTDS-----GSGGLFPDLP 52
DB 30 MDLFGDPEPERSPRPAKGEAKGGLFPDLPASSTDSGLQALPGSGGLFPDLP 89

QY 53 PASSGDSGLATSIQWVTEKGAKRKTSSEENKNGSELVEKVCASSVIFGLKGYA 112
DB 90 PASSGDSGLATSIQWVTEKGAKRKTSSEENKNGSELVEKVCASSVIFGLKGYA 149

QY 113 ERKGEEREMDVAIINDITEECRPSSLITRVSYFVDFGHCIRASKFAAQNHLNLI 172
DB 150 ERKGEEREMDVAIINDITEECRPSSLITRVSYFVDFGHCIRASKFAAQNHLNLI 209

QY 173 RKPPKGDVISE 184
DB 210 RKPPKGDVISE 221

LT 11
ABG07619
ID ABG07619 standard; Protein; 211 AA.
AC ABG07619;
DT 13-FEB-2002 (first entry)
DE Novel human diagnostic protein #7610.
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW Food supplement; medical imaging; diagnostic; genetic disorder.
OS Homo sapiens.
XX MO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT.
XX WPI, 2001-639362/73.
XX N-PSDB; AAS71806.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnosis, forensic, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID No 37978; 103pp; English.

The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensic, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification and was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 211 AA:

Query Match 26.4%; Score 533.5; DB 22; Length 211;
Best Local Similarity 61.4%; Pred. No. 2.6e-43;
Matches 124; Conservative 11; Mismatches 54; Indels 13; Gaps 5;

QY 204 KQASSQKPMW----KDSFATACVLAVDNITLYIANLGDSPA---ILCRVNEESQKHALSI 256
DB 10 RQNGSSKPLMLXGSGAOKSVYEVKPLLPQWIGHARRPCLQOACSSRPAPASL 69

QY 257 SKHNPTQYEEERWRIQ---KAGNVDRGVLGVEVSRISIDGOYKRCGVTSVPDIRRC 312
DB 70 PSSSPTARDTKHRAQVKTTDSGARRRDGRVIGVLEVSISADGGYKRCGVTSVPDIRRC 129

QY 313 QLTPTN-DRFILLACDGLFVFTPEEAVNIIISCLBDEKIQTEBGSAADARIEACNRLA 371
DB 130 QLTPOXGSLILACDGLFVFTPEEAVNIIISCLBDEKIQTEBGSAADARIEACNRLA 189

QY 372 NKAVORGS-ADNVTVMVVRIGH 392
DB 190 NKAVVAAGARPDNVTVMVVRIGH 211

RESULT 12
AAU23252
ID AAU23252 standard; Protein; 138 AA.
AC AAU23252;
DT 18-DEC-2001 (first entry)
DE Novel human enzyme polypeptide #338.
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX
XX Homo sapiens.
XX OS
XX PN WO200155301-A2.
XX
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US01239.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.

CC polynucleotides of the invention can also be used in gene therapy.
CC AAU22915-AAU23814 represent the novel human enzyme polypeptides of the
CC invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 138 AA;

Query Match 22.2%; Score 447.5; DB 22; Length 138;
Best Local Similarity 87.4%; Pred. No. 3.1e-35;
Matches 90; Conservative 1; Mismatches 11; Indels 1; Gaps 1;

Qy 279 RDGRVLGVLEVERISIGDQYKRCGVTSPDIRCOLTPNDRFILLACDGLFKVFTPEEAV 338
Db 10 RGRVGLGVLEVERISIGDQYKRCGVTSPDIRCOLTPNDRFILLACDGLFKVFTPEEAV 69

Qy 339 NFILSCLDEKIQTRREGKSAADARYEAACNRLANK-AVORGSA 380
70 NFILSCLDEKIQTRREGKSAADARYEAALQHAGQXGCSGRSA 112

RESULT 13

AAI8068
ID AAG18068 standard; Protein; 295 AA.

XX AAG18068;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 19329.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

PN EPI03405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

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RESULT 15

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DT 06-OCT-2000 (first entry)

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KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

XX gene therapy; chromosome mapping.

XX Homo sapiens.

PN EPI033401-A2.

PD 06-SEP-2000.

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PA Dumas Milne Edwards J, Duclert A, Giordano J;

PI WPI; 2000-500381/45.

DR N-PSDB; AAG03430.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

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XX Claim 13; SEQ ID 7505; 71bp + CD-ROM, English.
PS
XX

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CC The present sequence is a polypeptide encoded by one of a large number
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC were prepared from total human RNAs or polyA+ RNAs derived from 30'
CC different tissues. EST sequences usually correspond mainly to the 3'
CC untranslated region (UTR) of the mRNA because they are often obtained
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC those cases where longer cDNA sequences have been obtained, the full 5'
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC ends and can therefore be used to obtain full length cDNAs and genomic
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC chromosome mapping procedures. They are used to obtain upstream
CC regulatory sequences and to design expression and secretion vectors.
CC
XX
SQ

```

```

Query Match 20.0%; Score 404; DB 21; Length 86;
Best Local Similarity 92.9%; Pred. No. 2,5e-31;
Matches 79; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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QY 121 MODAHVILNDITEECRPPSSILITRVSYFAVFDGCGIRASKFAAQNLTQNLIRKPKGDV 180
Db 1 MODAHVILNDITEECRPPSSILITRVSYFAVFDGCGIRASKFAAQNLTQNLIRKPKGDV 180
QY 181 ISVEKTVKRCGLDPTFGHTDEEFLKQ 205
Db 61 ISVEKTVKRCGLDPTFGHTDEEFLKQ 205

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Search completed: June 7, 2003, 09:36:55
Job time : 41 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2003, 09:35:06 ; Search time 15 Seconds
(without alignments)
768.919 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018
Sequence: 1 MDLFDLDEBPRSPRPAK.....KAVRGADNVTVVVRIGH 392

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Issued Patents AA:*

- 1: /cgn2_6/ptodaca/1/1aa/SA_COMB.pep:*
- 2: /cgn2_6/ptodaca/1/1aa/SA_COMB.pep:*
- 3: /cgn2_6/ptodaca/1/1aa/SA_COMB.pep:*
- 4: /cgn2_6/ptodaca/1/1aa/SA_COMB.pep:*
- 5: /cgn2_6/ptodaca/1/1aa/SA_COMB.pep:*
- 6: /cgn2_6/ptodaca/1/1aa/SA_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2018	100.0	392	4	US-09-013-881-2
2	176	16.8	306	2	US-08-822-701-8
3	340	16.8	306	3	US-08-935-855-8
4	320.5	15.9	309	2	US-08-822-701-7
5	320.5	15.9	309	3	US-08-935-855-7
6	319	15.8	390	2	US-08-822-701-3
7	319	15.8	390	4	US-08-935-855-2
8	317.5	15.7	281	2	US-08-822-701-9
9	317.5	15.7	281	3	US-08-935-855-9
10	313	15.5	478	2	US-08-822-701-10
11	313	15.5	478	3	US-08-935-855-10
12	271.5	13.5	314	3	US-08-822-701-11
13	271.5	13.5	314	4	US-08-935-855-11
14	269.5	13.4	392	3	US-08-822-701-2
15	269.5	13.4	392	4	US-08-935-855-2
16	255.5	12.7	546	3	US-08-935-855-20
17	255.5	12.7	546	4	US-08-935-855-20
18	178	8.8	504	2	US-09-144-178-2
19	178	8.8	504	3	US-09-144-178-2
20	178	8.8	504	4	US-09-144-178-2
21	178	8.8	504	5	US-09-144-178-2
22	178	8.8	504	6	US-09-144-178-2
23	178	8.8	504	7	US-09-144-178-2
24	178	8.8	504	8	US-09-144-178-2
25	176	8.7	504	9	US-09-144-178-2
26	176	8.7	504	10	US-09-144-178-2
27	176	8.7	504	11	US-09-144-178-2

28	176	8.7	504	4	US-09-406-854-6
29	125	6.2	249	4	US-09-134-001C-4777
30	107	5.3	273	1	US-08-330-161-10
31	107	5.3	273	4	US-08-455-829-10
32	107	5.3	273	4	US-08-235-836C-13
33	107	5.3	273	4	US-08-455-923-10
34	103	5.1	475	4	US-09-370-838-193
35	100.5	5.0	466	4	US-08-235-836C-107
36	98.5	4.8	1085	1	US-08-431-080-28
37	96.5	4.8	1085	2	US-08-938-534-28
38	96.5	4.8	1085	4	US-09-345-294-28
39	95	4.7	447	4	US-09-916-109-5
40	95	4.7	483	4	US-09-916-109-5
41	94.5	4.7	422	2	US-09-067-351-3
42	94.5	4.7	422	4	US-09-360-490-3
43	92.5	4.6	2756	1	US-08-375-709-11
44	92.5	4.6	2756	1	US-08-752-929-11
45	92.5	4.6	2756	4	US-09-090-793-7

ALIGNMENTS

RESULT 1
US-09-013-881-2
Sequence 2, Application US/09013881
Patent No. 6132864
GENERAL INFORMATION:
APPLICANT: Bardman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Cortey, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Fuvri
TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSRO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,881
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0474 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNOT02
CLONE: 195647
US-09-013-881-2

Query Match 100.0%; Score 2018; DB 4; Length 392;
Best Local Similarity 100.0%; Pred. No. 6-8e-201;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPBPRPRAAGKEAGKGLPDDLPASTDSGSGPILFPDLPASSGDSG 60
DB 1 MDLFGDLPBPRPRAAGKEAGKGLPDDLPASTDSGSGPILFPDLPASSGDSG 60
QY 61 STATISOWKVTGKAKRKTSEENKNGSEBELVEKYCASSVIFGLKGVABRKGEREE 120
DB 61 STATISOWKVTGKAKRKTSEENKNGSEBELVEKYCASSVIFGLKGVABRKGEREE 120
QY 121 MODAHVILNDITEBCRPSSLITRVSYFAVFDHGIGIRASKFAAQLHQLIRKPKGDV 180
DB 121 MODAHVILNDITEBCRPSSLITRVSYFAVFDHGIGIRASKFAAQLHQLIRKPKGDV 180
QY 181 ISEKTVKRCCLDFTFKHTDEEFLKQASQKPAWKDSTATCVLAUNILYIANLGDSPAI 240
DB 181 ISEKTVKRCCLDFTFKHTDEEFLKQASQKPAWKDSTATCVLAUNILYIANLGDSPAI 240
QY 241 LCRVNESQKHAALSLSKENPTQYEEBMRIOKAGNVBDGVLGVLEVSRSIGDQYKR 300
DB 241 LCRVNESQKHAALSLSKENPTQYEEBMRIOKAGNVBDGVLGVLEVSRSIGDQYKR 300
QY 301 CGVTSVPDIRRCQLTENDREFILLACDGLPKVFTPEBAVNFILSCLEDEKIQTRREGKSAAD 360
DB 301 CGVTSVPDIRRCQLTENDREFILLACDGLPKVFTPEBAVNFILSCLEDEKIQTRREGKSAAD 360
QY 361 ARYEACNRLANKAVORGSAADNTVMVVRIGH 392
DB 361 ARYEACNRLANKAVORGSAADNTVMVVRIGH 392

RESULT 2

US-08-822-701-8
Sequence 8, Application US/08822701
Patent No. 5976853

GENERAL INFORMATION:

APPLICANT: Guthridge, Mark
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FINI3
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Rattus
US-08-822-701-8

Query Match 16.8%; Score 340; DB 2; Length 306;
Best Local Similarity 33.7%; Pred. No. 6e-27;
Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

QY 106 GLKGYAERKGEREEMQAHVILNDITEBCRPSSLITRVSYFAVFDHGIGIRASKFAAQL 165
DB 21 GLRYGLSSWQGVREMEDAHTAVIGL-----PSGLET-WSPFAVYDGHAGSQVAKYCE 73
QY 166 NIHLNLIKRP-KED--VISVEKTVKRCCLDFTFKHTDEEFLKQASQKPAWKDSTATCV 222
DB 74 HLDDHITNNQDFKSGAGAPSYE-NVKNIGIRTFGLIDEHMRVMSKKGAGADSGSTAVGV 132
QY 223 LAVNDILYIANLGDSPAILCRVNESQKHAALSLSKENPTQYEEBMRIOKAGNVBDGR 282
DB 133 LISPHITFINGDSDRLCR-----NRKVHFTQDKPSNPLEKERIQNAGSVMIOR 186
QY 283 VLGVLVSRISIDGQYKRC---GVT-----SVPIRRCQLTENDREFILLACDGLFK 330
DB 187 VNGSLAVSRALDGFYK-CVHGKGFTQLVSPPEVHDIERSE--EDQFILLACDGIWD 243
QY 331 VFTPEBAVNFILSCLE--DEKIQTRREGKSAADARYEACNRLANKAVORGSAADNTVMV 388
DB 244 VNGNEELCDPFVRSRLVETD-----LEKVCNEVVDTCLYKSGSHDMSVILI 289

RESULT 3

US-08-935-855-8
Sequence 8, Application US/08935855
Patent No. 6066485

GENERAL INFORMATION:

APPLICANT: Guthridge, Mark
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FINI3
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: Rattus
 US-08-935-855-8

Query Match 16.8%; Score 340; DB 3; Length 306;
 Best Local Similarity 33.7%; Pred. No. 6e-27;
 Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

QY 106 GLKGVAEKREEMODAHVILNDITECRPPSSLTIVSYFAVFDHGIGIRASKFAAQ 165
 DB 21 GLRYGLSSMOGWREMEDAHVAVGL-----PSGLET-WSPFAVYDGHASQVAKYCE 73
 QY 166 NLHONLIRKP-KGD--VISYEKTVKRCLLDTPFKHTDEEFLKQASSOKPAWKDSTATCV 222
 DB 74 HLDHITNNODFKSGAGAPSYE--NVKNGIRTFLEIDEIMRWSEKKGADRSOSTAVGV 132
 QY 223 LAVDNILYIANIGDSRALICRYNEESOKHAALSLSEKHNPTQYEEERMRIOKAGNVADGR 282
 DB 133 LISPHQTYFINCGDSRGLICR-----NRKVHFPTQDHKPSNPLEKERIQVAGGSVMIOE 186
 QY 283 VLGVLEVSRSIGDGGYKRC---GVT-----SYPDIRRCQLTNPNDRIILACDGLPK 330
 DB 187 VNGSLAVSRALGDIFYK-CVAGKGPFGQIVSPPEVHDIERE--EDDQFIILACGIMD 243
 QY 331 VFTPEAVNFILSCLE--DEKIQTRBKSAADARVACNPLANKAVORGADNVYVWV 368
 DB 244 VMGNELCDPVSRLVETD-----LEKVCNEVVOICLYKSRDMNSVILI 289

RESULT 4
 US-09-206-646-4
 Sequence 4, Application US/09206646
 Patent No. 643637
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Goli, Surya K.
 APPLICANT: Lal, Preeti G.
 APPLICANT: Corley, Neil C.
 APPLICANT: Zhang, Hong
 TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
 FILE REFERENCE: PF-0319-1 DIV
 CURRENT APPLICATION NUMBER: US/09/206,646
 CURRENT FILING DATE: 2001-12-07
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PERL Program
 SEQ ID NO 4
 LENGTH: 390
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: ID No. 6436637 g452526
 US-09-206-646-4

Query Match 16.2%; Score 326; DB 4; Length 390;
 Best Local Similarity 30.0%; Pred. No. 2.5e-25;
 Matches 98; Conservative 52; Mismatches 121; Indels 56; Gaps 10;

QY 78 KRRTSEKNGSEELVEKVKKASVIFGLKGVAEKREEMODAHVILNDITECRP 137
 DB 7 KPTTEKNAHAGN-----GLRYGLSSMOGWREMEDAHVAVGI----- 46
 QY 138 PSSLITVSYFAVFDHGIGIRASKFAAONLHONL-----IRKPK-GDVI--SVEKTVR 189
 DB 47 PHGL-DNWSFFAVYDGHASRVANVCSHLEHITTEDFRAADSGSALSPSYE-SVKT 104
 QY 190 CLDTPFKHTDEEFLKQASSOKPAWKDSTATCVLAVDNILYIANIGDSRALICRYNEEQ 249
 DB 105 GIRTGLKIDIEYMRNFSDLRNGMDRSSTAVGVWSPHMYFINCGDSRAVLCSNQG--- 161

QY 250 KHAALSLSEKHNPTQYEEERMRIOKAGNVADGRVILGVLEYSREIGDGGYKRCG----- 302
 DB 162 ---VCFSTQHKRCNVEKERIQNAGSGVMIOQVNGSLAVSRALGDIFYKCDGSGPTQ 218
 QY 303 -VTSVPDIRRCQLTNPNDRIILACDGLFKVTPPEANFILTSGDEBKIQTRBKSAADA 361
 DB 219 LVSPPEVETVVAEDEFVILACDGIWDVNSNELCEFKVKNLE-----VSD 266
 QY 362 RYEAACRLANKAVORGADNVYVWV 388
 DB 267 DLENVCNVVDTCLHKGRDMSVVLV 293

RESULT 5
 US-08-822-701-7
 Sequence 7, Application US/08822701
 Patent No. 597683
 GENERAL INFORMATION:
 APPLICANT: Guthridge, Mark
 APPLICANT: Basilio, Claudio
 TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
 TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/822,701
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-002 N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 309 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: Mus musculus
 US-08-822-701-7

Query Match 15.9%; Score 320.5; DB 2; Length 309;
 Best Local Similarity 29.7%; Pred. No. 6.5e-25;
 Matches 98; Conservative 54; Mismatches 115; Indels 63; Gaps 12;

QY 78 KRRTSEKNGSEELVEKVKKASVIFGLKGVAEKREEMODAHVILNDITECRP 137
 DB 7 KPTTEKNAHAGN-----GLRYGLSSMOGWREMEDAHVAVGI----- 46
 QY 138 PSSLITVSYFAVFDHGIGIRASKFAAONLHONL-----IRKPK-GDVI--SVE--KTV 187
 DB 47 PHGL-DNWSFFAVYDGHASRVANVCSHLEHITTEDFRAADSGSALSPSYEVSXKG 105
 QY 186 KRCLDTPFKHTDEEFLKQASSOKPAW-KDGSATATCVLAVDNILYIANIGDSRALICRYNE 246

Db 106 RTGFLKI-----DEYKRNFSDLRNGMDRSGSTAAGVWVSPTTHMYFINCGSRALCRNGQ 160
QY 247 ESQKHAALSKEHNPTQYEERMRIQKAGNVRDGVLTGLEVSRISIGGOYKRCG-----302
Db 161 -----VCFSTQDHKPCNPVEKERIQVAGSVMIQKRVNSLAVSRALGDIYKCVDGKGP 214
QY 303 ----VTSVPDIRCOLTPNDRFILACDGLFKVFTPEEAVNFILSCLEDEKIQTEGKSA 358
Db 215 TEQVSPPEPEVEIYVRAEDEFVVLACDGIWDMVMSNEELCEFKSRLE-----262
QY 359 ADARYEACNRLANKAVQGSADNTVMVY 388
Db 263 VSDLENCVMVYDTCLHKGRDNMSVILV 292

RESULT 6
US-08-935-855-7
Sequence 7, Application US/08935855
Patent No. 6066485

GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FINI3
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Mus musculus

US-08-935-855-7

Query Match 15.9%; Score 320.5; DB 3; Length 309;
Best Local Similarity 29.7%; Pred. No. 6,5e-25;
Matches 98; Conservative 54; Mismatches 115; Indels 63; Gaps 12;

QY 78 KRKTSEENKGESEELVEKVKCASSVIFGLKGYAERKGEREEMODAHVILNDITECRP 137
Db 7 KRKTSEENKGESEELVEKVKCASSVIFGLKGYAERKGEREEMODAHVILNDITECRP 46
QY 138 PSSLLTRVYFAVFDGHRGIRASKFAAQLHONL-----IRKFPK-GDVI--SVE--KTV 187

Db 47 PHGL-DNMSFAVYDGHAGSRVANYCSTILLEHTTNEDEFRADKSGSALBESVESVKTG 105
QY 188 KCLLDTFKHTDEEFLKQASSOKPAM-KDGSTATCVLANDNLTLYIANIGDSRAILCRVNE 246
Db 106 RTGFLKI-----DEYKRNFSDLRNGMDRSGSTAAGVWVSPTTHMYFINCGSRALCRNGQ 160
QY 247 ESQKHAALSKEHNPTQYEERMRIQKAGNVRDGVLTGLEVSRISIGGOYKRCG-----302
Db 161 -----VCFSTQDHKPCNPVEKERIQVAGSVMIQKRVNSLAVSRALGDIYKCVDGKGP 214
QY 303 ----VTSVPDIRCOLTPNDRFILACDGLFKVFTPEEAVNFILSCLEDEKIQTEGKSA 358
Db 215 TEQVSPPEPEVEIYVRAEDEFVVLACDGIWDMVMSNEELCEFKSRLE-----262
QY 359 ADARYEACNRLANKAVQGSADNTVMVY 388
Db 263 VSDLENCVMVYDTCLHKGRDNMSVILV 292

RESULT 7
US-08-873-093-3
Sequence 3, Application US/08873093
Patent No. 5853997

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1247927

US-08-873-093-3

Query Match 15.8%; Score 319; DB 2; Length 390;
Best Local Similarity 29.4%; Pred. No. 1.3e-24;
Matches 96; Conservative 51; Mismatches 124; Indels 56; Gaps 9;

QY 78 KRKTSEENKGESEELVEKVKCASSVIFGLKGYAERKGEREEMODAHVILNDITECRP 137

```

Db      7 KPKTEKHNAGN-----GLRYGLSSMOGWRVEMEDAHAVVGI-----46
Oy      138 PSSLIIRVSYFVAFDGHGIRASFAAONLHQL-----IRKFPKGVY---SVEKTVR 189
Db      47 PHGL-EDMSFFAVVDGAGSIVANYCSTHLEHTTNEDEFRADSSGPALEPSVE-NVKT 104
Oy      190 CLIDTFKHTDEEFLKQASSOKPAKMGSTATCVLAVDNILYANIGDSRAILCRVNEBQ 249
Db      105 GIRTGFLKIDETMRNFSDLRNGMRSGSTIVGMSPTHTIYINGDSRAVLCRNGQ---161
Oy      250 KHAALSLSEKHNPTOYERMRNIQAGGNVDGVLGVTEVSRISGDOGYRCG-----302
Db      162 ---VCFSTODHKPCNPEKERIQWAGSVMICQVNSLAVALGDYKCVDGKPTQ 218
Oy      303 -VTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRKGSADA 361
Db      219 LVSPEPEVEYLRAEDEFVVLACDGIWDMSNBELCEPVNSRLE-----VSD 266
Oy      362 RYEAACNRLANKAVORGASADVTVTVV 388
        267 DLENVCNMYVDTCLHKSGRDMISIVL 293

```

RESULT 8

```

US-09-206-646-3
: Sequence 3, Application US/09206646
: Patent No. 643637
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Goli, Surti K.
: APPLICANT: Gali, Preeti G.
: APPLICANT: Corley, Neil C.
: APPLICANT: Zhang, Hong
: TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
: FILE REFERENCE: PF-0319-1 DIV
: CURRENT APPLICATION NUMBER: US/09/206,646
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PERL Program
: SEQ ID NO 3
: LENGTH: 390
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: OTHER INFORMATION: ID No. 643637 9247927
US-09-206-646-3

```

Query Match 15.8%; Score 319; DB 4; Length 390;

Best Local Similarity 29.4%; Pred. No. 1.3e-24; Matches 96; Conservative 51; Mismatches 124; Indels 56; Gaps 9;

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Oy      78 KRRTSEKNGSEELVEKVKCASVIFGLKGVVAERKGERENMODAHVILNDITECRP 137
Db      7 KPKTEKHNAGN-----GLRYGLSSMOGWRVEMEDAHAVVGI-----46
Oy      138 PSSLIIRVSYFVAFDGHGIRASFAAONLHQL-----IRKFPKGVY---SVEKTVR 189
Db      47 PHGL-EDMSFFAVVDGAGSIVANYCSTHLEHTTNEDEFRADSSGPALEPSVE-NVKT 104
Oy      190 CLIDTFKHTDEEFLKQASSOKPAKMGSTATCVLAVDNILYANIGDSRAILCRVNEBQ 249
Db      105 GIRTGFLKIDETMRNFSDLRNGMRSGSTIVGMSPTHTIYINGDSRAVLCRNGQ---161
Oy      250 KHAALSLSEKHNPTOYERMRNIQAGGNVDGVLGVTEVSRISGDOGYRCG-----302
Db      162 ---VCFSTODHKPCNPEKERIQWAGSVMICQVNSLAVALGDYKCVDGKPTQ 218
Oy      303 -VTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRKGSADA 361
Db      219 LVSPEPEVEYLRAEDEFVVLACDGIWDMSNBELCEPVNSRLE-----VSD 266
Oy      362 RYEAACNRLANKAVORGASADVTVTVV 388

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Db      267 DLENVCNMYVDTCLHKSGRDMISIVL 293

```

RESULT 9

```

US-08-822-701-9
: Sequence 9, Application US/08822701
: Patent No. 5976853
: GENERAL INFORMATION:
: APPLICANT: Guttridge, Mark
: APPLICANT: Basilico, Claudio
: TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESS: David A. Jackson, Esq.
: STREET: 411 Hackensack Ave, Continental Plaza, 4th
: STREET: Floor
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/822,701
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REGISTRATION NUMBER: 26,742
: REFERENCE/DOCKET NUMBER: 1049-1-002 N
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-487-5800
: TELEFAX: 201-343-1684
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 281 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEICAL: NO
: FRAGMENT TYPE:
: ORIGINAL SOURCE:
: ORGANISM: Saccharomyces cerevisiae
US-08-822-701-9

```

Query Match 15.7%; Score 317.5; DB 2; Length 281;

Best Local Similarity 31.4%; Pred. No. 1.1e-24; Matches 95; Conservative 44; Mismatches 93; Indels 71; Gaps 12;

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Oy      111 VAERKGE--REEMODAHVILNDITECRPSSLIIRV--SYPAVFDGHGIRASFAAON 166
Db      23 VAENKNSKFRITMEDVHTVKNFA-----SRIDMGYFVAFDGHGIRASFAAON 72
Oy      167 LH-----ONLIRKFPKGVYSEKTVKRCCLDTFNGHDEEFLKQASSOKPAKMGST-ATC 221
Db      73 LHITIEONIT-----ADETRDVRLVNSFPAIDEEI-----NTKLVGNSGCTAAVC 119
Oy      222 VL---AVDNI-----LYIANIGDSRAILCRVNEBQKHAALSLSEKHNPTQY 265
Db      120 VLRLNELPDSVSDMSMDLAHQKRYTANVGDSTRIVLFRNN-----SIRLYDHRKASDT 173
Oy      266 EEMRIQKAGGNVDGVLGVTEVSRISGDOGYRCGVTSVPDIRCOLTPNDRFILLAC 325
Db      174 LEMGRVQAGGLIMKSRVNGMLAVTRSLGDKFFDSLTVGS-PFTTSVEITSEDKFLILAC 232
Oy      326 DGLFKVFTPEEAVNFILSCLEDEKIQTRKGSADAARVEACNRLANKAVORGASADVTV 385

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Oy      250 KHAALSLSKENHPVOYEEMRILOKAGVAVDGRVLGVLEWSSRIDQCYKRRCG-----30Z
              ::|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      162 ----VCFTSQDHKKPCNPEKERIONNGSGVMIOFVNGLVASBALDYDKCVDDKPTEQ   218
Oy      303 -VTVPDIRRQCQLPNDPRFILACCGLFKYTPPEAIVNFILSCLEDERIQTRBSKAADA    361
              |||:|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      219 LVSPPREVEYLAEDEDFILLACCIGIDWNDSNELCEYVKRL- -----VSD       266
Oy      362 RYAACNRPLANKAVOGSADNTWWVV     388
Db      267 DLENVGMVDCTLHKSRSDNNSTLV     293

RESULT 12
US-08-873--093-4
; Sequence 4, Application US/08873093
; Patent No. 5853997
; GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Indocyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873_093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1452526
? :
? :
US-08-873--093-4

Query Match          15.5%; Score 313; DB 2; Length 478;
Best Local Similarity 28.7%; Pred. No. 7, Re-24;
Matches           94; Conservative 52; Mismatches 125; Indels 56; Gaps 8
```

US-08-822-701-10
Sequence 10, Application US/08822701 1
Patent No. 5976853
GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
SERINE/THREONINE PHOSPHATASE, FINI3
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Leishmania
US-08-822-701-10

Query Match 13.5%; Score 271.5; DB 2; Length 314;
Best Local Similarity 28.0%; Pred. No. 8e-20; Indels 83; Gaps 12;
Matches 84; Conservative 43; Mismatches 90;

116 GEREEMODAHVILNDITECRPPSSLITRVSYFAVFDGIGIRASGFAAONLHONLIRKF 175
116 GEREEMODAHVILNDITECRPPSSLITRVSYFAVFDGIGIRASGFAAONLHONLIRKF 175
31 GYREIMEDHNL-----TYLTDWMGFGVFDGIVNDQCGOYLERARRS----- 72
176 PKGDVIVSEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKD-----GSTATCVLAVDN--- 227
73 -----ALEK-----ESIPMTDERMKEALRIDQEMWDSGREGSGTGFVALKEGNNK 119
228 -LLYIANLGDSPAILCRYNESQKHAALSKEHNPTQYEEMRIKAGGNVRDGRVIGV 286
120 VHLQVGNVDSRVAC-----IDGVCVPLTEDHKPNNEGERORLNCAGRVENNRVDS 173
287 LEVSRISIGGOYK-----RCGVTSVPDIRCQLT--PNDRFILLACDGLFK-VFTPEE 336
174 LAVSRAFGREYKLGSGOLEQKVIYALADVQHKDTFDSND-FVLLCCDGVEGNFPNPE 232
337 AVNFIILSCLEDEKIOTREGKSAADARYEACN-----RLANKAVQGSADNVTVVVR 389
233 VVAIVKQOLE-----TCNDLAEVAGRVCEBAIERGSRDNISCMIVQ 273

RESULT 15
US-08-935-855-10

Sequence 10, Application US/08935855
Patent No. 6066485
GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
SERINE/THREONINE PHOSPHATASE, FINI3
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Leishmania
US-08-935-855-10

Query Match 13.5%; Score 271.5; DB 3; Length 314;
Best Local Similarity 28.0%; Pred. No. 8e-20; Indels 83; Gaps 12;
Matches 84; Conservative 43; Mismatches 90;

116 GEREEMODAHVILNDITECRPPSSLITRVSYFAVFDGIGIRASGFAAONLHONLIRKF 175
116 GEREEMODAHVILNDITECRPPSSLITRVSYFAVFDGIGIRASGFAAONLHONLIRKF 175
31 GYREIMEDHNL-----TYLTDWMGFGVFDGIVNDQCGOYLERARRS----- 72
176 PKGDVIVSEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKD-----GSTATCVLAVDN--- 227
73 -----ALEK-----ESIPMTDERMKEALRIDQEMWDSGREGSGTGFVALKEGNNK 119
228 -LLYIANLGDSPAILCRYNESQKHAALSKEHNPTQYEEMRIKAGGNVRDGRVIGV 286
120 VHLQVGNVDSRVAC-----IDGVCVPLTEDHKPNNEGERORLNCAGRVENNRVDS 173
287 LEVSRISIGGOYK-----RCGVTSVPDIRCQLT--PNDRFILLACDGLFK-VFTPEE 336
174 LAVSRAFGREYKLGSGOLEQKVIYALADVQHKDTFDSND-FVLLCCDGVEGNFPNPE 232
337 AVNFIILSCLEDEKIOTREGKSAADARYEACN-----RLANKAVQGSADNVTVVVR 389
233 VVAIVKQOLE-----TCNDLAEVAGRVCEBAIERGSRDNISCMIVQ 273

Search completed: June 7, 2003, 09:37:41
Job time: 17 secs